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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=25; hr=17; min=43; sec=12; ms=958;]

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Reviewer Comments:

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

The above <120> response exceeds the Sequence Rules' required 72-character limit per line (this includes white spaces). Please insert a hard return after "SCREENING."

<210> 5

<211> 291

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(291)

<223>

<220>

<221> sig_peptide

<222> (1)..(81)

<223>

<220>

<221> mat_peptide

<222> (82)..()

<223>

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Met	Ala	Cys	Gly	Gly	Lys	Arg	Leu	Leu	Phe	Leu	Ala	Leu	Ala	Trp	Val	
	-25						-20							-15		
ctg	ctg	gct	cac	ctc	tgc	agc	cag	gca	gaa	gca	gca	agc	aac	tac	gac	96
Leu	Leu	Ala	His	Leu	Cys	Ser	Gln	Ala	Glu	Ala	Ala	Ser	Asn	Tyr	Asp	
	-10					-5			-1	1					5	
tgt	tgc	ctc	tcg	tac	ata	cag	acg	cct	ctt	cct	tcc	aga	gct	att	gtg	144
Cys	Cys	Leu	Ser	Tyr	Ile	Gln	Thr	Pro	Leu	Pro	Ser	Arg	Ala	Ile	Val	
		10					15							20		
ggt	ttc	aca	aga	cag	atg	gcc	gat	gaa	gct	tgt	gac	att	aat	gct	atc	192
Gly	Phe	Thr	Arg	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile	
		25					30						35			
atc	ttt	cac	acg	aag	aaa	aga	aaa	tct	gtg	tgc	gct	gat	cca	aag	cag	240
Ile	Phe	His	Thr	Lys	Lys	Arg	Lys	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln	
		40					45						50			
aac	tgg	gtg	aaa	agg	gct	gtg	aac	ctc	ctc	agc	cta	aga	gtc	aag	aag	288
Asn	Trp	Val	Lys	Arg	Ala	Val	Asn	Leu	Leu	Ser	Leu	Arg	Val	Lys	Lys	
		55					60						65			
atg																291
Met																

70 In the above last line, "70" is not properly aligned under "Met," the last amino acid. Same type of error in Sequence 7.

Application No: 10547532 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
W 112	Upper case found in data; Found at position(291) SeqId(5)
E 259	Found undefined lettercode; POS (293) SEQID(5)
E 254	The total number of bases conflicts with running total, Input: 70, Calculated : 294 SEQID(5)
E 253	The number of bases differs from <211> Input: 291 Calculated:294
E 201	Mandatory field data missing in <223> in SEQ ID (7)
W 112	Upper case found in data; Found at position(1122) SeqId(7)
E 259	Found undefined lettercode; POS (1124) SEQID(7)
W 112	Upper case found in data; Found at position(1125) SeqId(7)
E 259	Found undefined lettercode; POS (1127) SEQID(7)
W 112	Upper case found in data; Found at position(1128) SeqId(7)

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
E 259	Found undefined lettercode; POS (1130) SEQID(7)
W 112	Upper case found in data; Found at position(1131) SeqId(7)
E 259	Found undefined lettercode; POS (1134) SEQID(7)
W 112	Upper case found in data; Found at position(1134) SeqId(7)
W 112	Upper case found in data; Found at position(1137) SeqId(7)
E 259	Found undefined lettercode; POS (1139) SEQID(7)
E 254	The total number of bases conflicts with running total, Input: 370, Calculated : 1140 SEQID(7)
E 253	The number of bases differs from <211> Input: 1122
E 201	Mandatory field data missing in <223> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
E 201	Mandatory field data missing in <223> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (15)
E 201	Mandatory field data missing in <223> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10547532

<141> 2008-01-17

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(288)

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<222> (1)...(78)

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<221> mat_peptide

<222> (79)...()

<223>

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atg tgc tgt acc aag agt ttg ctc ctg gct gct ttg atg tca gtg ctg 48

Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu

-25 -20 -15

cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc 96

Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys

-10 -5 -1 1 5

tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc 144

Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly

10 15 20

ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc 192

Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act 240
 Phe His Thr Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50
 tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg 288
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

 <210> 2
 <211> 96
 <212> PRT
 <213> Homo sapiens

 <400> 2
 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 -25 -20 -15
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 -1 1 5
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 Phe His Thr Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

 <210> 3
 <211> 288
 <212> DNA
 <213> Rattus norvegicus

 <220>
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 <222> (1)..(288)
 <223>

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 <221> sig_peptide
 <222> (1)..(75)
 <223>

 <220>
 <221> mat_peptide
 <222> (76)..()
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 -25 -20 -15 -10
 gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc 96
 Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
 -5 -1 1 5
 ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt 144
 Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly

10	15	20	
ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc			192
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile			
25	30	35	
ttt cac ctg aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc			240
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile			
40	45	50	55
tgg gtg aaa agg att ttg cac ctc ctc agc cta aga acc acc aag aag atg			288
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met			
60	65	70	

<210> 4
 <211> 96
 <212> PRT
 <213> Rattus norvegicus

<400> 4			
Met Ala Cys Lys His Leu Pro Phe Leu Ala Leu Ala Gly Val Leu Leu			
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Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys			
-5	-1	1	5
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly			
10	15	20	
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile			
25	30	35	
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile			
40	45	50	55
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met			
60	65	70	

<210> 5
 <211> 291
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(291)
 <223>

<220>
 <221> sig_peptide
 <222> (1)...(81)
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<220>
 <221> mat_peptide
 <222> (82)...()
 <223>

<400> 5			
atg gcc tgc ggt ggc aag cgt ctg ctc ttc ctt gct ttg gca tgg gta			48
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-25	-20	-15	
ctg ctg gct cac ctc tgc agc cag gca gaa gca gca agc aac tac gac			96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp			
-10	-5	-1	1
			5

tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg	144
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val	
10 15 20	
ggt ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc	192
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile	
25 30 35	
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag	240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln	
40 45 50	
aac tgg gtg aaa agg gct gtg aac ctc ctc acg cta aga gtc aag aag	288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys	
55 60 65	
atg	291
Met	70

<210> 6
<211> 97
<212> PRT
<213> *Mus musculus*

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-10 -5 -1 1 5	
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val	
10 15 20	
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile	
25 30 35	
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln	
40 45 50	
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys	
55 60 65	
Met	
70	

<210> 7
<211> 1122
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1)...(1122)
<223>

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gat tat ttt gtg tca gtc aat act tca tat tac tca gtt gat tct gag	96
Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu	
20 25 30	
atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt	144
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe	
35 40 45	

gta ccg att gcc tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat		192
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn		
50 55 60		
att ctg gtg atc acc ttt gct ttt tat aag aag gcc agg tct atg		240
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met		
65 70 75 80		
aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt		288
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val		
85 90 95		
ctt act ctc cca ttc tgg gca gtg agt cat gcc act ggt gcg tgg gtt		336
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val		
100 105 110		
ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac		384
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn		
115 120 125		
ttt aac tgc ggg atg ctg ctc ctg act tgc att agc atg gac cgg tac		432
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr		
130 135 140		
atc gcc att gta cag gcg act aag tca ttc cgg ctc cga tcc aga aca		480
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr		
145 150 155 160		
cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc		528
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val		
165 170 175		
atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa		576
Ile Ile Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln		
180 185 190		
ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc		624
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile		
195 200 205		
agg tgg aag ctg ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt		672
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe		
210 215 220		
atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att gtc aaa acc		720
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr		
225 230 235 240		
ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc		768
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile		
245 250 255		
ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg		816
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met		
260 265 270		
gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc tgc		864
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys		
275 280 285		
cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa gtc ctg		912
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu		
290 295 300		
gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg		960
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly		
305 310 315 320		
cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt		1008
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys		
325 330 335		
gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac		1056
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr		
340 345 350		

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Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn		
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gcg tcg tcc ttc act atg		1122
Ala Ser Ser Phe Thr Met		370

<210> 8
 <211> 374
 <212> PRT
 <213> Homo sapiens

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Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe			
35	40	45	
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn			
50	55	60	
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met			
65	70	75	80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val			
85	90	95	
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val			
100	105	110	
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn			
115	120	125	
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr			
130	135	140	
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr			
145	150	155	160
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val			
165	170	175	
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln			
180	185	190	
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile			
195	200	205	
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe			
210	215	220	
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr			
225	230	235	240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile			
245	250	255	
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met			
260	265	270	
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys			
275	280	285	
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu			
290	295	300	
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly			
305	310	315	320
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys			
325	330	335	
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr			
340	345	350	

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355 360 365
Ala Ser Ser Phe Thr Met
370

<210> 9
<211> 1101
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1101)
<223>

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gag tat tat tct att cct cca gac cat ggg cca tgc tcc cta gaa gag 96
Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
20 25 30
gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta ata 144
Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
35 40 45
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Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
50 55 60
ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg aac atg 240
Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
65 70 75 80
gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288
Ala Ile Thr